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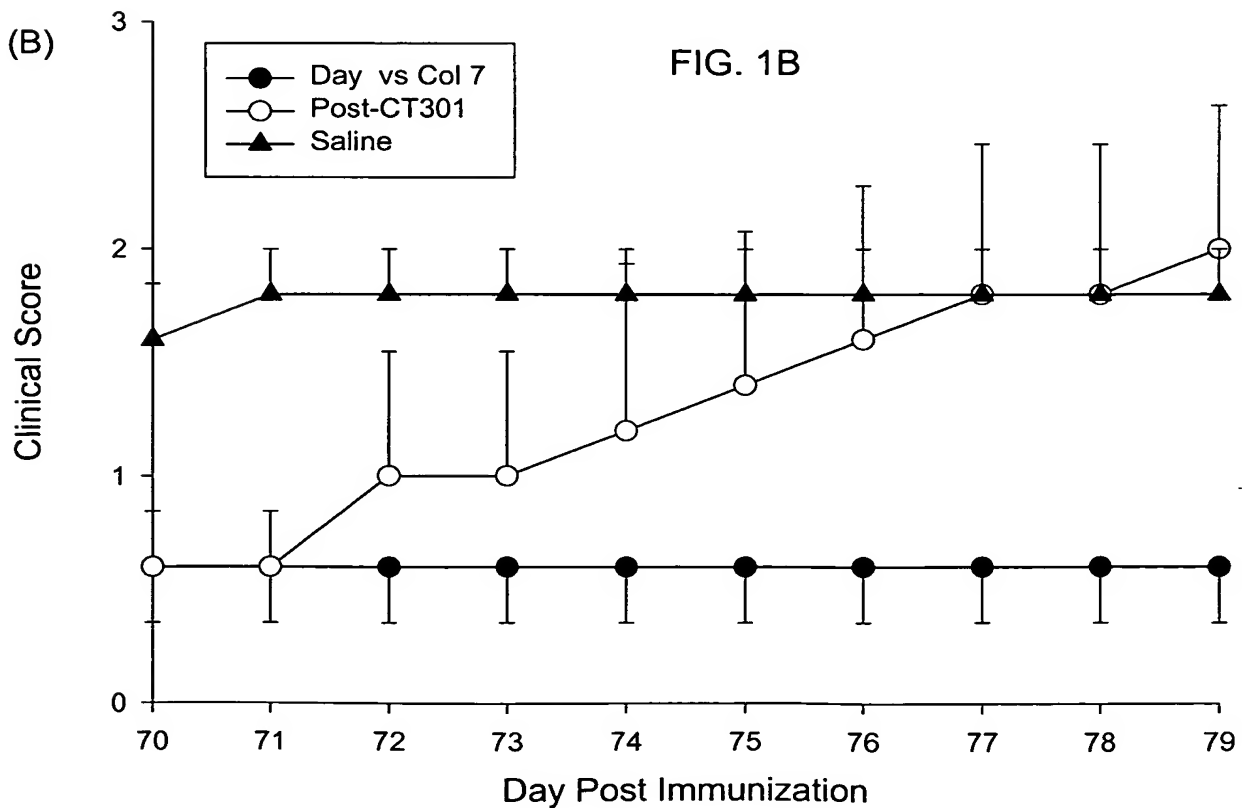
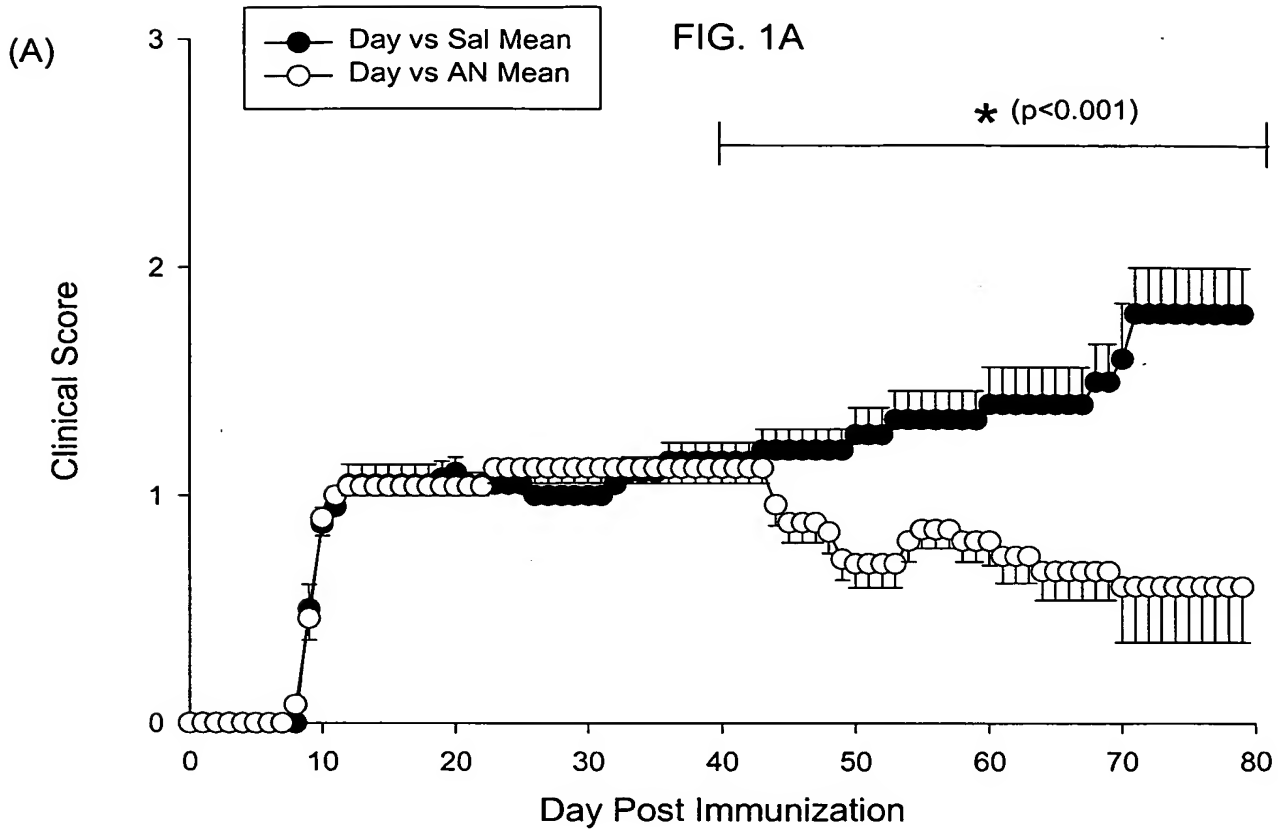




FIG. 2G

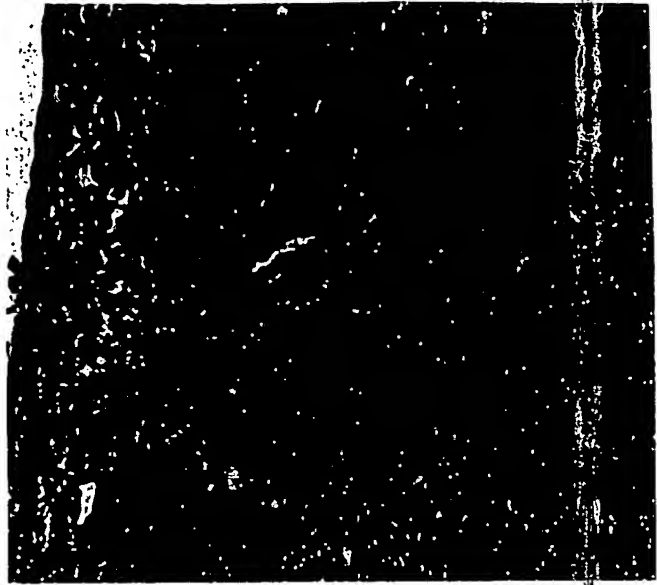


FIG. 2H

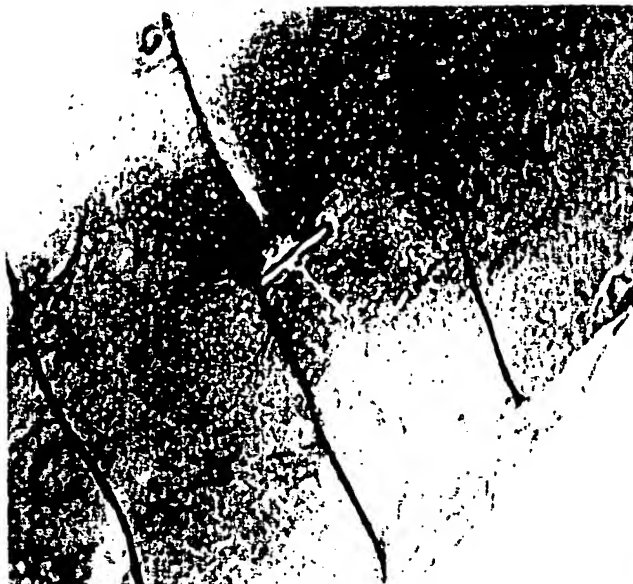


FIG. 2I

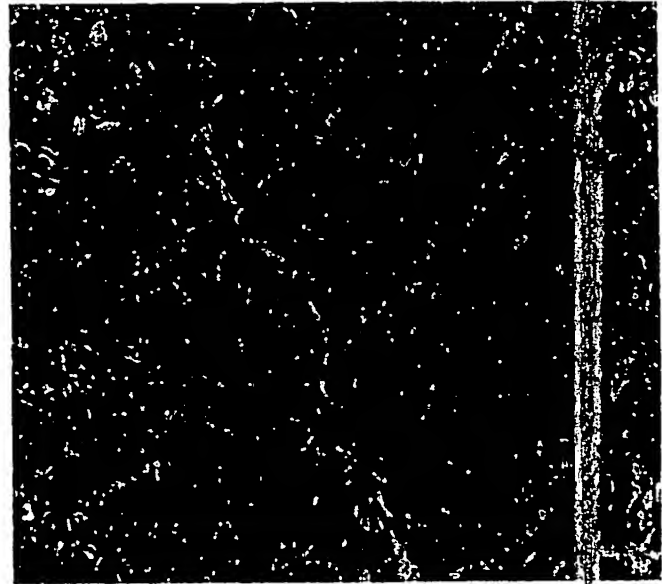


FIG. 2J



FIG. 2K

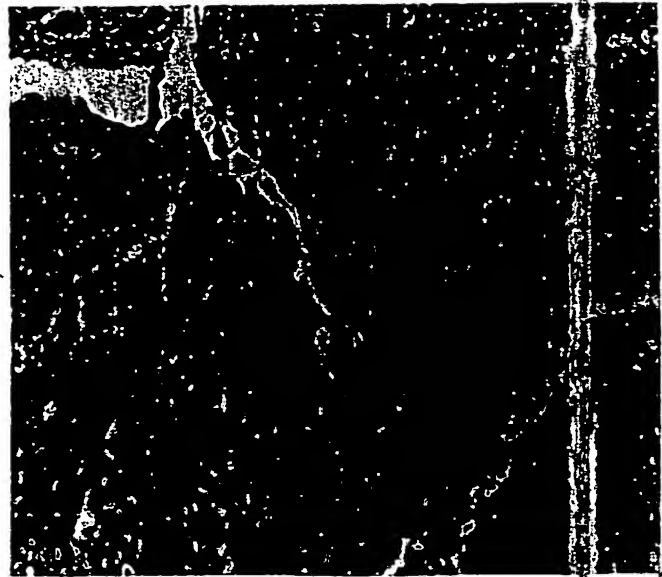


FIG. 2L



FIG. 2A

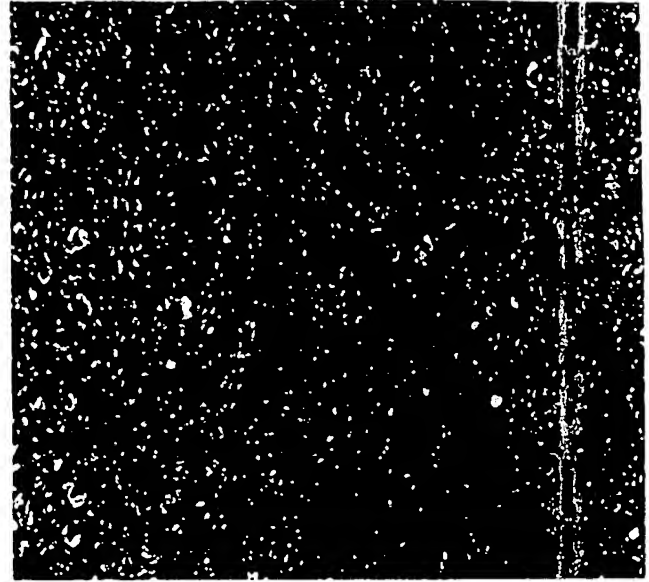


FIG. 2B

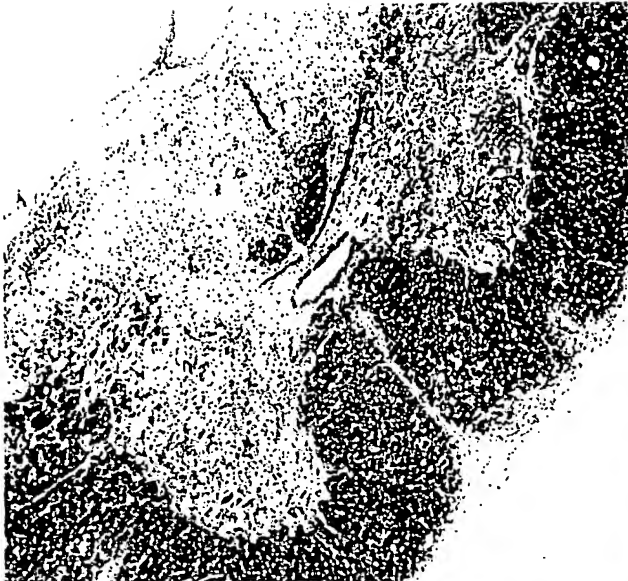


FIG. 2C

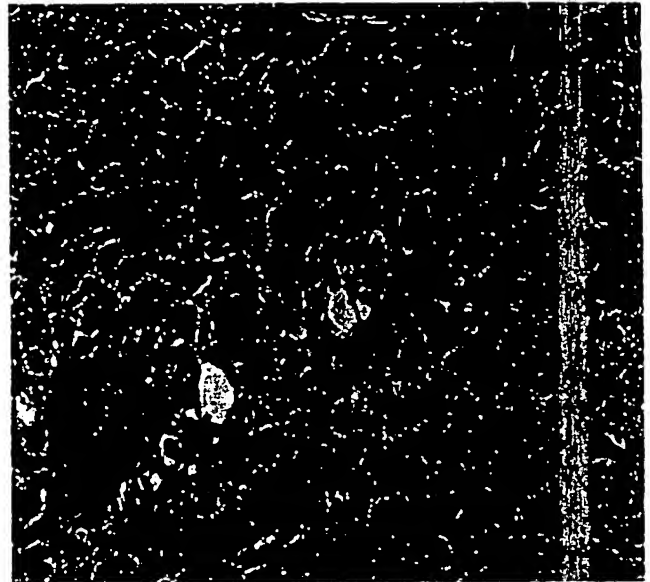


FIG. 2D



FIG. 2E

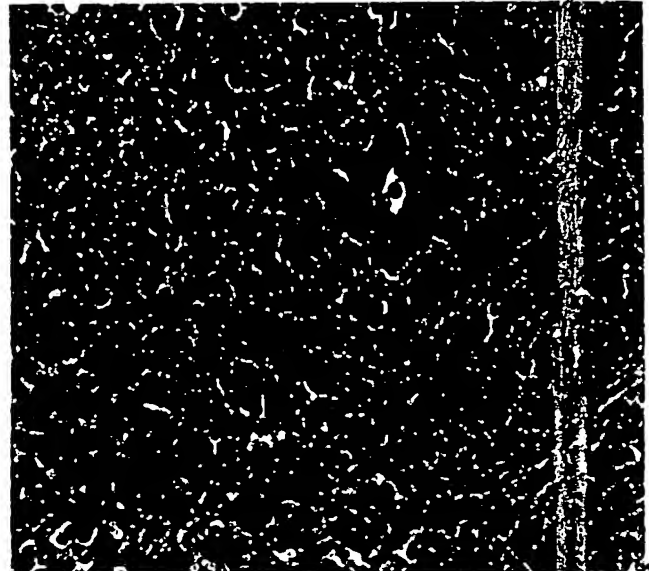
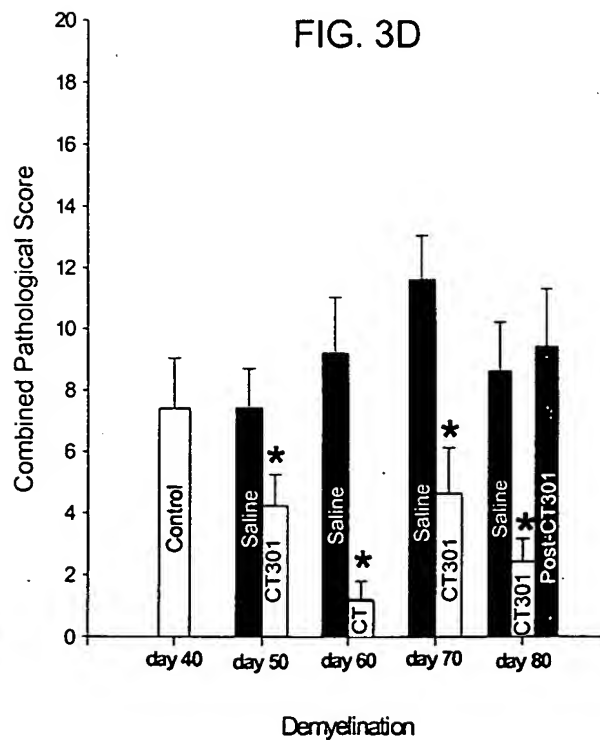
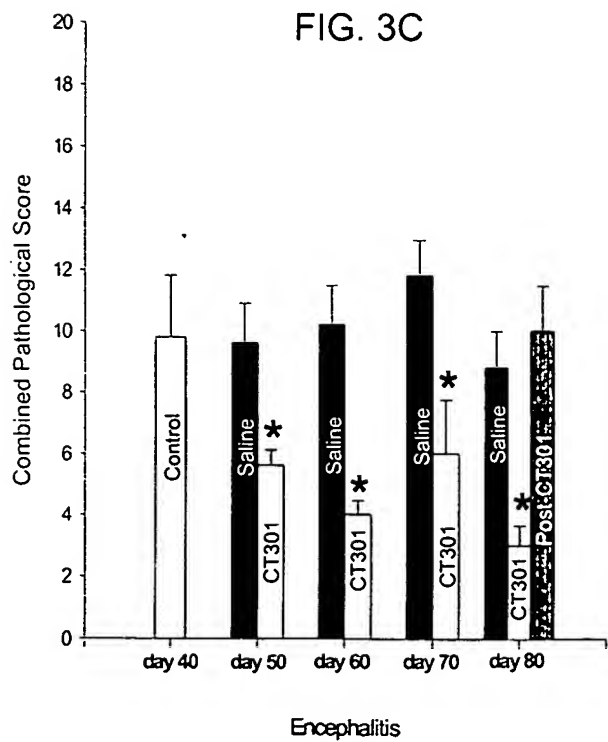
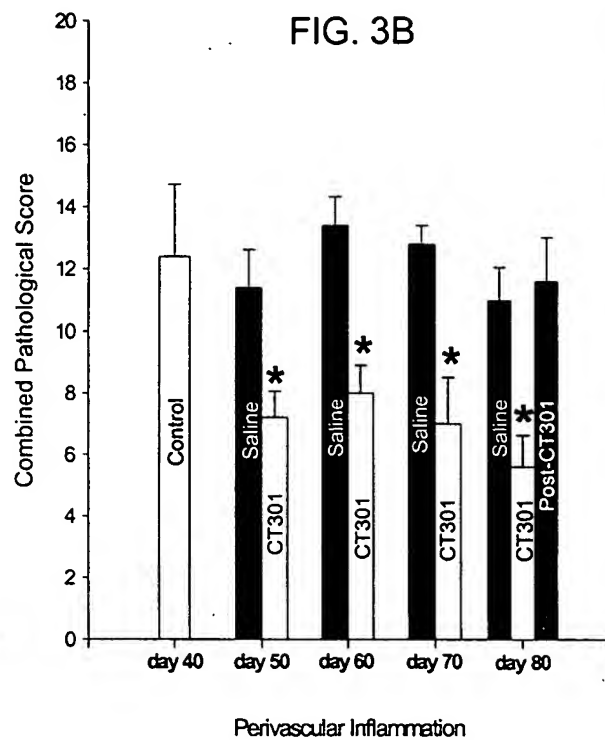
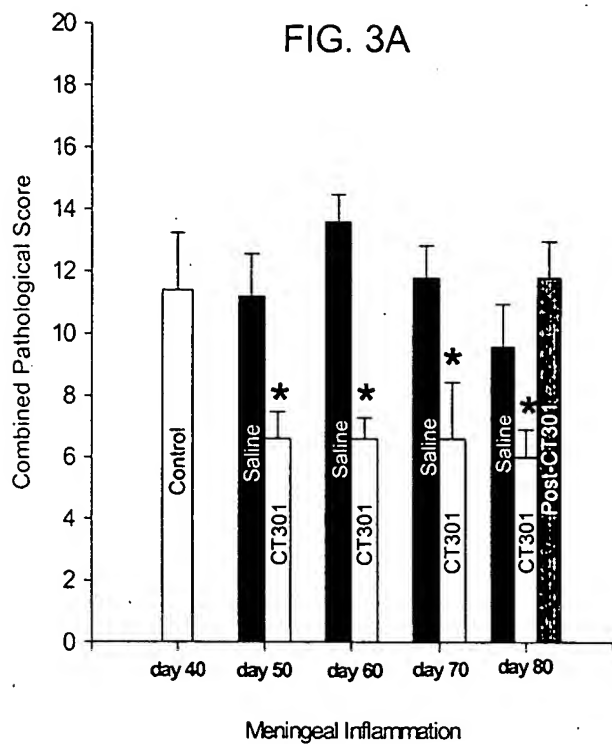


FIG. 2F



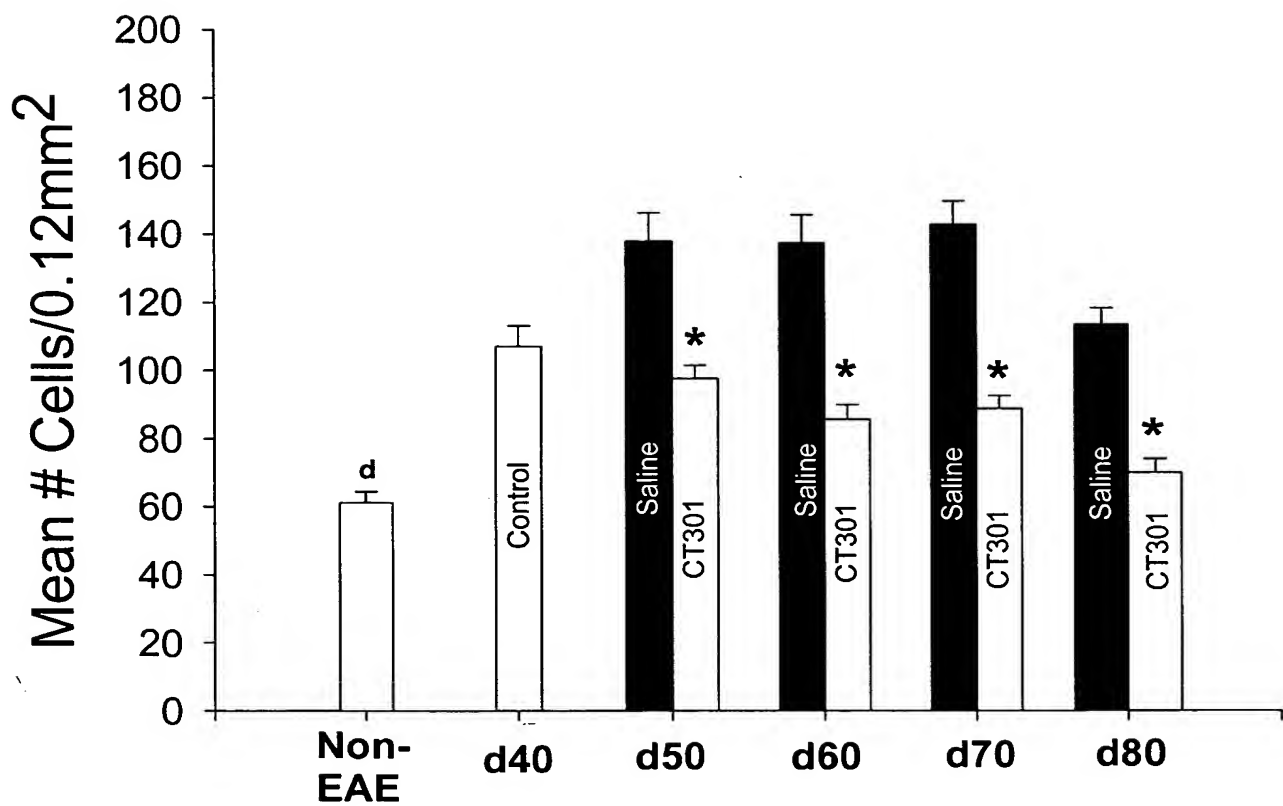
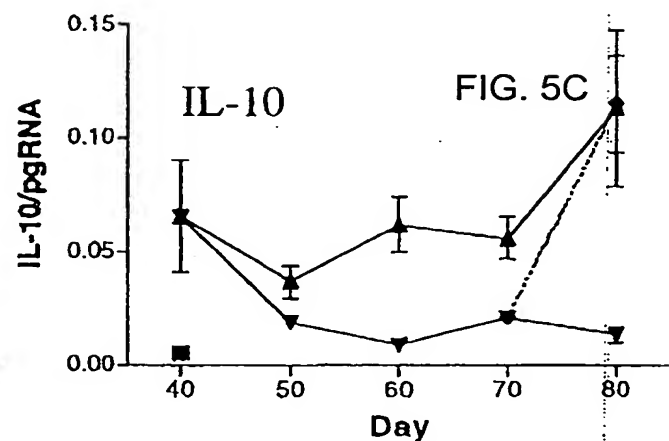
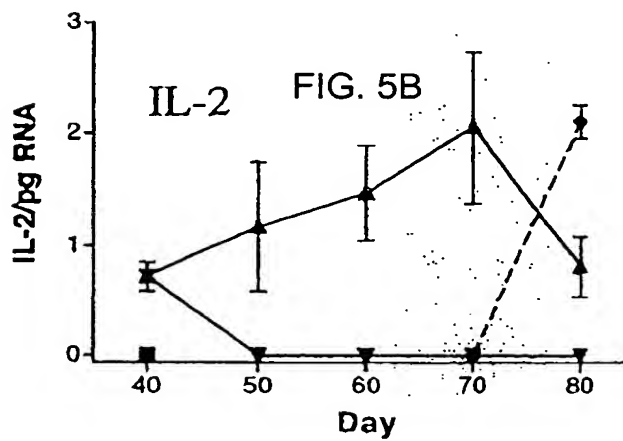
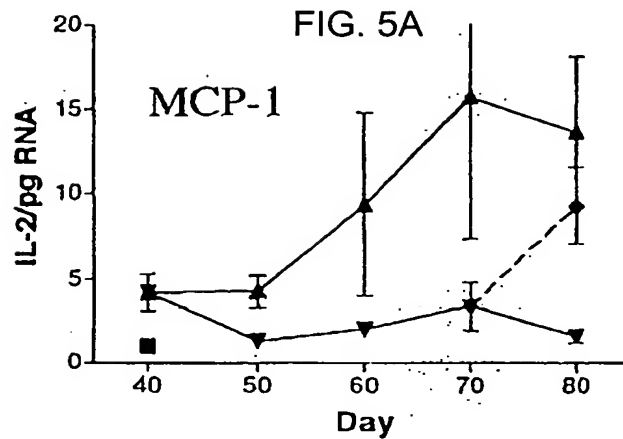
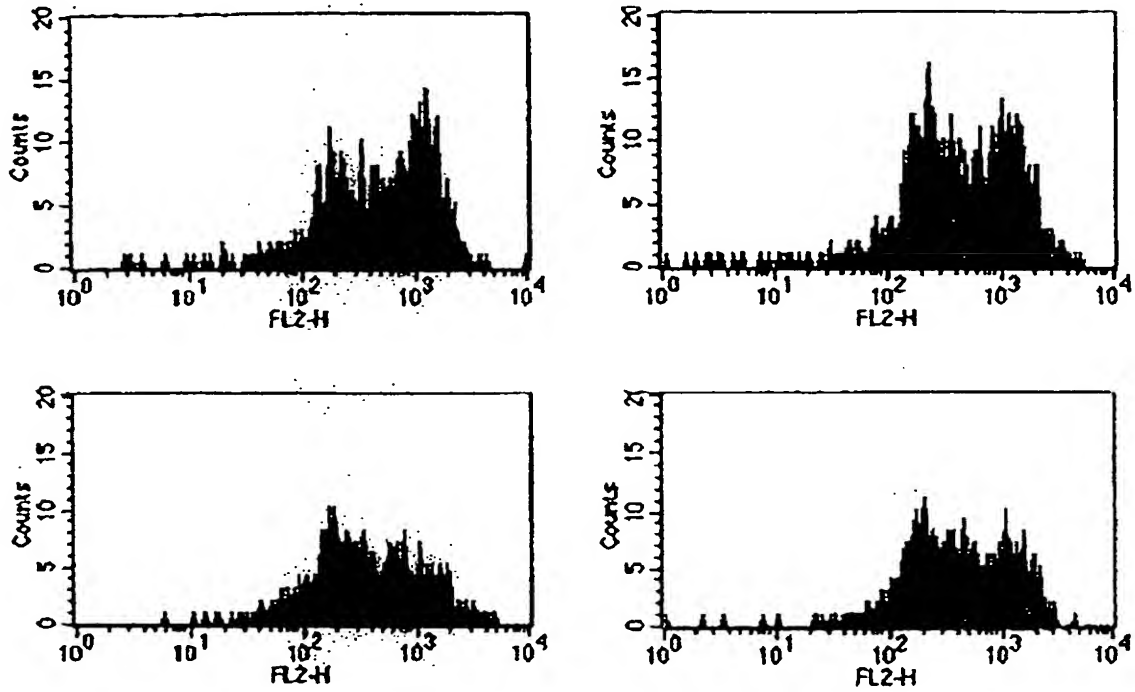


FIG. 4



CT301



Saline

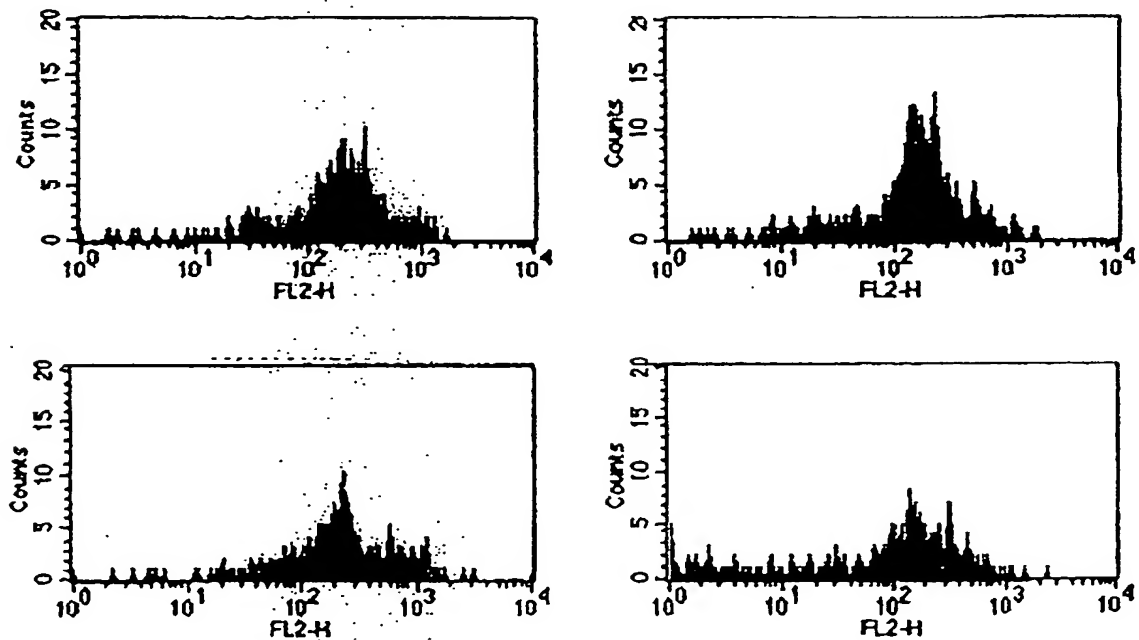


FIG. 6

Percentage $\alpha 4$ Integrin-High Blood Lymphocytes

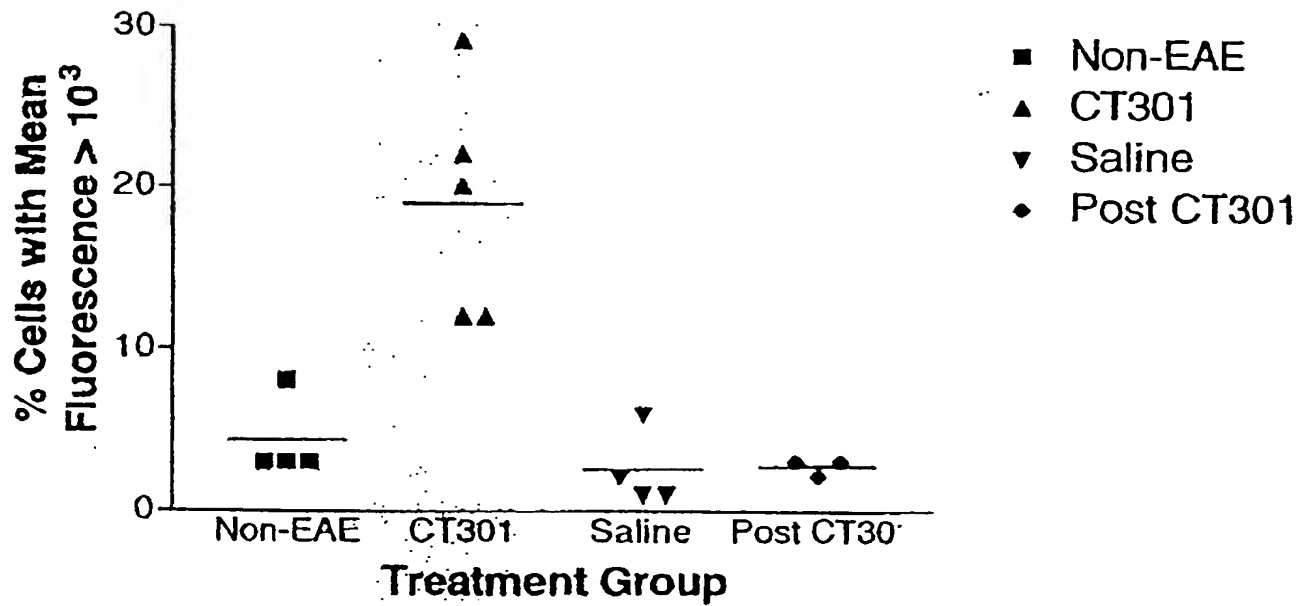


FIG. 7A

Expression of $\alpha 4$ Integrin on Blood Monocytes

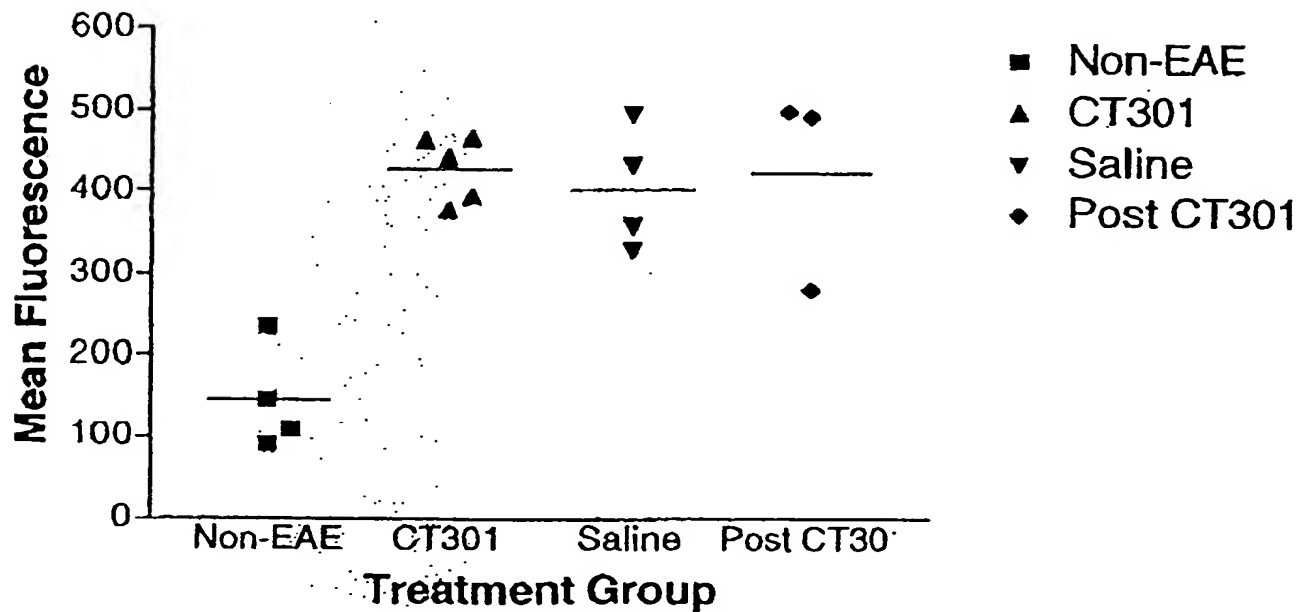


FIG. 7B

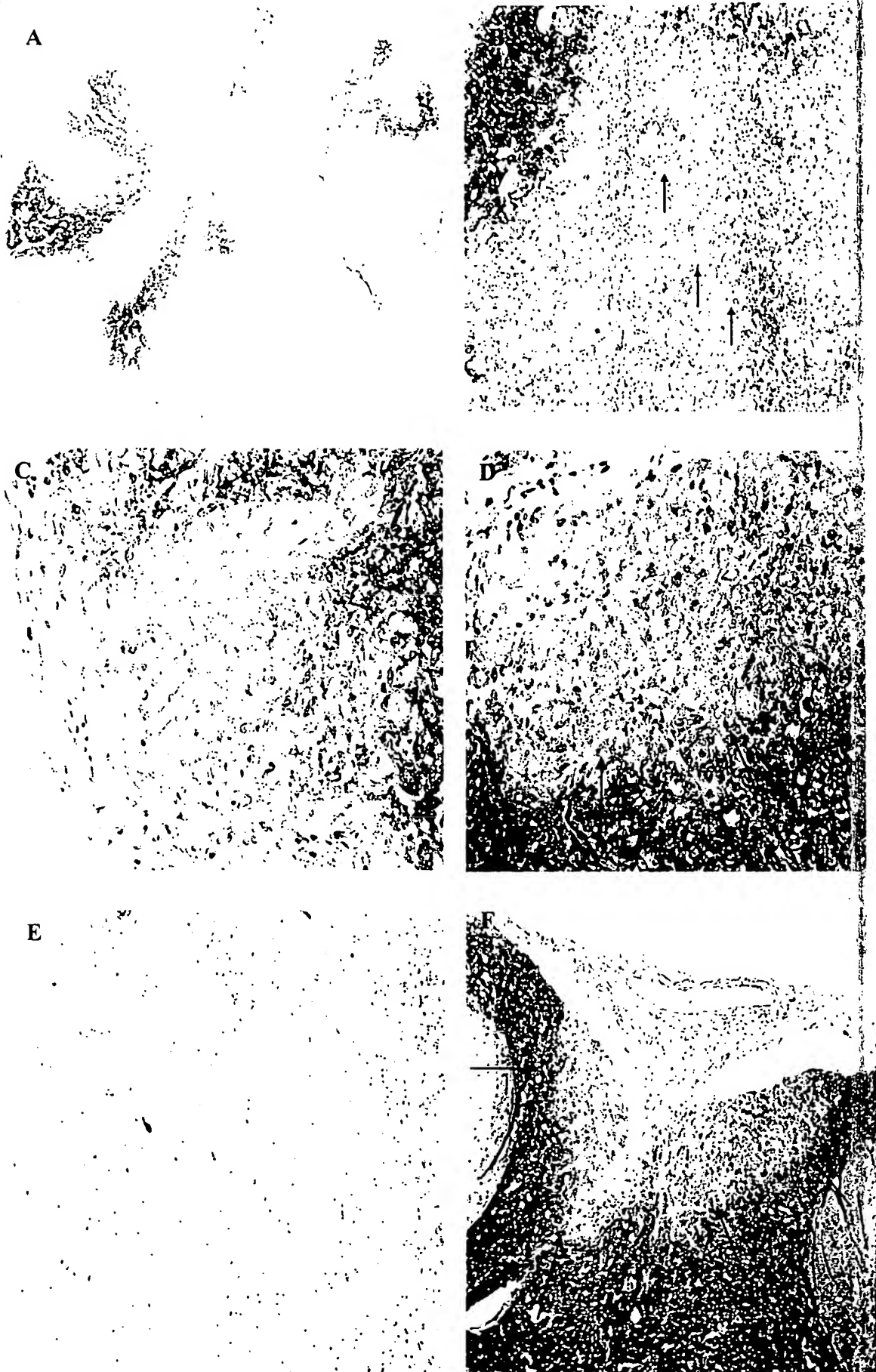


FIG. 8

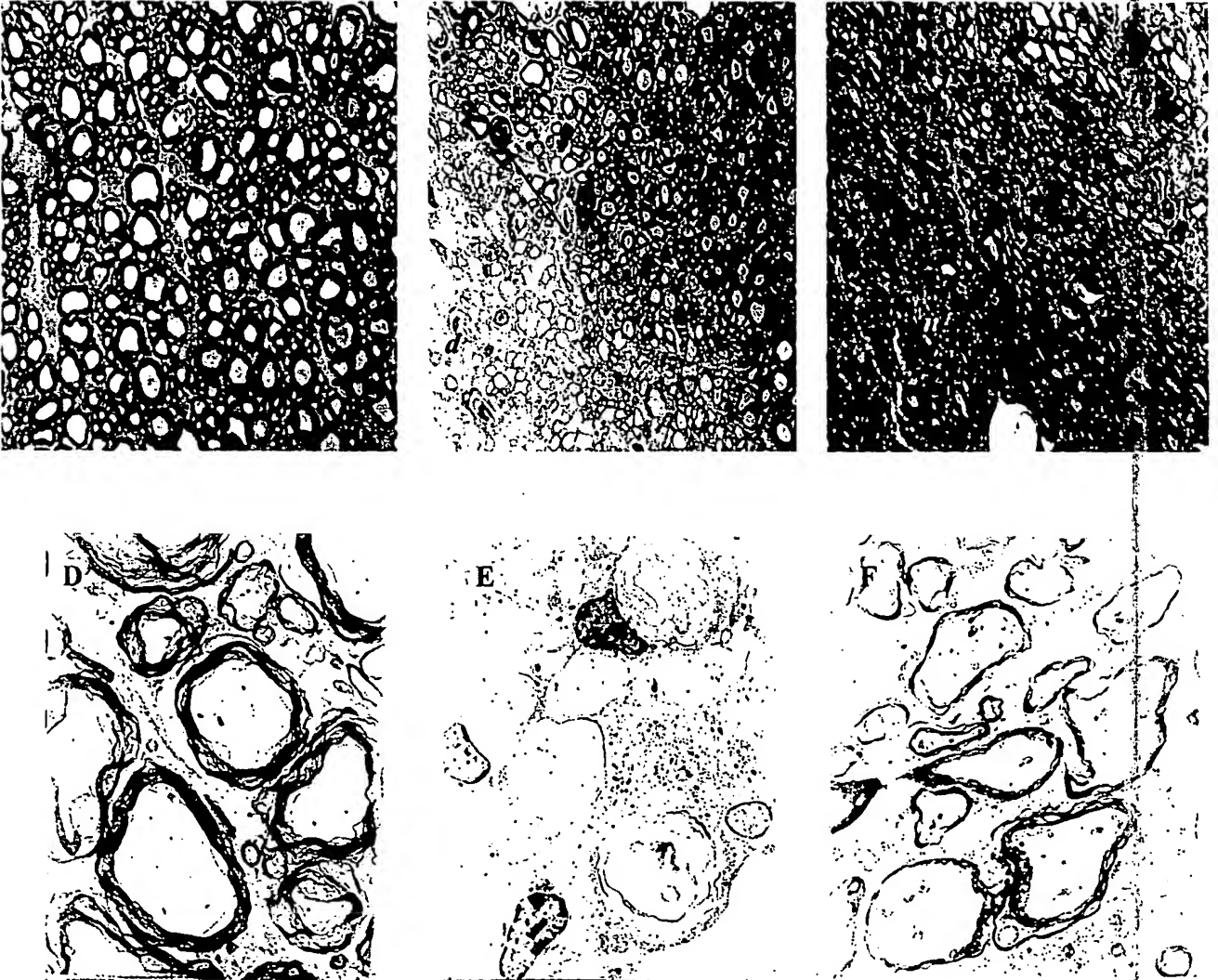


FIG. 9

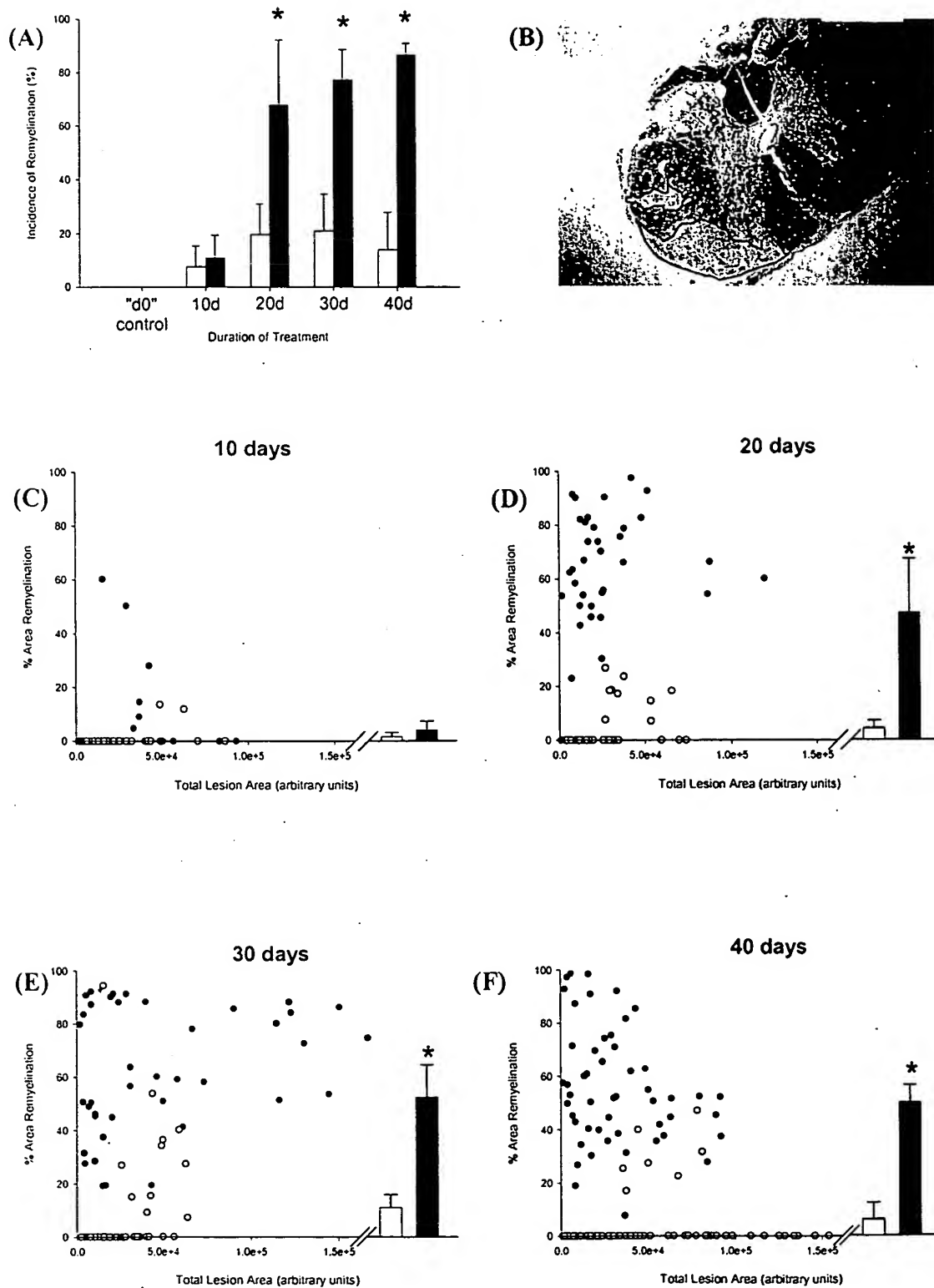


FIG. 10

1 atgagggccctgctcagatttttggattcttggtcaggagacgttgt

tactcccggggacgagctctaaaaacctaagaaccagtcctctgcaaca

49 agaaatgagaccgtctattcagttcctggggctcttgttgttctggcttcatgg

tctttactctggcagataagtcaaggaccccgagaacaacaagaccgaagtacc
[M R P S I Q F L G L L L F W L H G
LEADER

103 tgctcagtggtgacatccagatgacacagtcctccatcctcactgtctgcatctct

acgagtcacactgtaggtctactgtgtcagaggtaggagtgacagacgtagaga
A Q C][D I Q M T Q S P S S L S A S L
FR1

157 gggaggcaagtccaccatcacttgcaagacaagccaagacattaacaagtatat

ccctccgtttcagtggttagtgaacgttctgttcggttctgtaattgttcatata
G G K V T I T C][K T S Q D I N K Y M
CDR1

211 ggcttggtaccaacacaagcctggaaaacgtcctagggtgctcatacattacac

ccgaaccatggttgtgttcggaccttttgcaggatccgacgagtatgtaattgtg
A][W Y Q H K P G K R P R L L I H][Y T
FR2

265 atctgcattacagccaggcatcccatcaagggttcagtggaagtgggtctgggag

tagacgtaatgtcggccgtagggtagttccaagtcaccttcacccagaccctc
S A L Q P][G I P S R F S G S G S G R
CDR2

FIG. 11 A

319 agattattccttcaacatcagcaacctggagcctgaagatattgcaacttatta

tctaataaggaagttgtagtcggttgacctcggacttctataacggtgaataat

D Y S F N I S N L E P E D I A T Y Y
FR3

373 ttgtctacagtatgataatctgtggacggttcggtggaggcaccaagctggaaat

aacagatgtcatactattagacacctgcaagccacctcgtggttcgacctta

C)[L Q Y D N L W T][F G G G T K L E I
CDR3 FR4

427 caaacgggctgatgctgcaccaactgtatccatcttcccaccatccaccggga

gtttgcccgactacgacgtggttgacataggtagaaggggtggtaggtggccct

K)

AGG-5'
tcc
481 ---
agg

FIG. 11B

1 atgaaatgcagctgggtcatgttcttcctgatggcagtggttacaggg

tactttacgtcgacccagtacaagaaggactaccgtcaccaatgtccc

[M K C S W V M F F L M A V V T G
LEADER

49 gtcaattcagagggttcagctgcagcagctctggggcagagcttgtgaagccaggg

cagttaagtctccaagtcgacgtcgtcagaccccgctctcgaacacttcggtccc
V N S][E V Q L Q Q S G A E L V K P G
FR1

103 gcctcagtcgaagttgtcctgcacagcttctggcttcaacattaaagacacctat

cggagtcagttcaacaggacgtgtcgaagaccgaagttgtaatttctgtggata
A S V K L S C T A S G F N I K][D T Y
CDR1

157 atacactgtgtgaagcagaggcctgaacagggcctggagtggttgaaggatt

tatgtgacacacttcgtctccggacttgtcccggacctcacctaaccttcctaa
I H][C V K Q R P E Q G L E W I G][R I
FR2

211 gatcctgcgaatgggttataactaaatatgacccgaagttccagggcaaggccact

ctaggacgcttaccaatatgatttatactgggcttcaaggtcccgttccggtga
D P A N G Y T K Y D P K F Q G][K A T
CDR2

265 ataacagctgacacatcctccaacacagcctacctgcagctcagcagcctgaca

tattgtcgactgtgtaggaggttgtgtcggatggacgtcgagtcgtcggactgt
I T A D T S S N T A Y L Q L S S L T
FR3

FIG. 12A

319 tctgaggacactgccgtctatttctgtgctagagagggatattatggtaactac

agactcctgtgacggcagataaagacacgatctctccctataataaccattgatg
S E D T A V Y F C A R] [E G Y Y G N Y
CDR3

373 ggggtctatgctatggactactggggtcaaggaacctcagtcaccgtctcctca

ccccagatacagatacctgatgaccccgattccttggagtcagtggcagaggagt
G V Y A M D Y] [W G Q C T S V T V S S]

427 gccaaaacgacacccccatctgtctatccactggcccgggatcc

cggttttgctgtgggggtagacagataggtgaccgggcccctagg
S S]

FIG. 12B

| | FR1 | CDR1 | FR2 | CDR2 |
|------|-------------------------|-------------|-----------------|---------|
| | 1 | 2 | 3 | 4 |
| | 5 | 6 | 7 | 8 |
| | 12345678901234567890123 | 45678901234 | 567890123456789 | 0123456 |
| | * | ***** | * | *** |
| 21.6 | DIQMTQSPSSLSASLGKVTITC | KTSQDINKYMA | WYQHKPGKRPRLLIH | YTSALQP |
| REI | DIQMTQSPSSLSASVGDRVTITC | QASQDIIKYLN | WYQQTGKAPKLLIY | EASNLQA |
| La | DIQMTQSPSSLSASVGDRVTITC | KTSQDINKYMA | WYQQTGKAPBLLIH | YTSALQP |
| Lb | -----R----- | | | |

| | FR3 | CDR3 | FR4 |
|------|------------------------------------|-----------|------------|
| | 6 | 7 | 8 |
| | 9 | 10 | 11 |
| | 78901234567890123456789012345678 | 901234567 | 8901234567 |
| | * | * | ***** |
| 21.6 | GIPSRFSGSGSGRDYSFNISNLEPEDIATYYC | LQYDNL-WT | FGGGTKLEIK |
| REI | GVPSRFSGSGSGTDYFTFTISSLQPEDIAATYYC | QQYQSLPYT | FGQGTLQIT |
| La | GIPSRFSGSGSGRDYFTFTISSLQPEDIAATYYC | LQYDNL-WT | FGQGTKVEIK |
| Lb | -I-----R-----VE-K | | |

FIG. 13

| | FR1 | | | | | | | | | | CDR1 | | | | | | | | | | FR2 | | | | | | | | | | CDR2 | | | | | | | | | |
|------|--------------------------------|------------|------------|------------|------------|-------|-------|-----------|--------------|-------|-------------|-------|----------------|--|--|---|--|-------------------|--|--|-----|--|--|--|--|---|------|--|--|--|------|--|--|--|--|--|--|--|--|--|
| | 1 | | | | | 2 | | | | | 3 | | | | | 4 | | | | | 5 | | | | | 6 | | | | | | | | | | | | | | |
| | 1234567890 | 1234567890 | 1234567890 | 1234567890 | 1234567890 | 12345 | 67890 | 123456789 | 012A34567890 | 12345 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | ***** | *** | | | | | | | | | | | | | | | **** | | | | | | | | | | | | | |
| 21.6 | EVQLQQSGAELVKPGASVKLSCTASGFNIK | | | | | | | | | | | DTYIH | CVKQRPEQGLEWIG | | | | | RIDPANGYTKYDPKFQG | | | | | | | | | | | | | | | | | | | | | | |
| 2*CL | QVQLVQSGAEVKKPGASVKVSKASGYTFT | | | | | | | | | | | SYAMH | WVRQAPGQRLEWMG | | | | | WINAGNGNTKYSQKFQG | | | | | | | | | | | | | | | | | | | | | | |
| Ha | QVQLVQSGAEVKKPGASVKVSKASGENIK | | | | | | | | | | | DTYIH | WVRQAPGQRLEWMB | | | | | RIDPANGYTKYDPKFQG | | | | | | | | | | | | | | | | | | | | | | |
| Hb | -----FNIK | | | | | | | | | | -----G----- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Hc | -----FNIK | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

| | 7 | 8 | 9 | 10 | 11 |
|------|----------------------------------|----------------|-----------------|-------|--------|
| | 67890123456789012ABC345678901234 | 567890ABCDEF12 | 345678901234 | | |
| 21.6 | KATITADTSSNTAYLQLSSLTSED | TAVYFCAR | EGYYGNYGVIYAMDY | WGQGT | SVTVSS |
| 2*CL | RVTITRDTSASTAYMELSSLRSED | TAVYYCAR | GGYYGSGS---- | NY | WGQGT |
| Ha | RVTITADTSASTAYMELSSLRSED | TAVYYCAR | EGYYGNYGVIYAMDY | WGQGT | SVTVSS |
| Hb | -----A----- | ----- | ----- | ----- | ----- |
| Hc | -----A----- | ----- | ----- | ----- | ----- |

FIG. 14

HindIII KOZAK SEQUENCE

```

1  aagcttgccgccaccatgagaccgtctattcagttcctggggctcttggtgttc
   -----
   ttccaacggcggtggtactctggcagataagtcaaggaccccgagaacaacaag

           [ M R P S I Q F L G L L L F
                                LEADER

55  tggcttcattggtgctcagtgtgacatccagatgacacagtctccatcctcactg
   -----
   accgaagtaccacgagtcacactgtagggtctactgtgtcagaggtaggagtgac

   W L H G A Q C ] [ D I Q M T Q S P S S L
                                FR1

109 tctgcatctGTAggaGATAGAgtcaccatcacttgcaagacaagccaagacatt
   -----
   agacgtagaCATcctCTATCTcagtggtagtgaacggttctgttcgggttctgtaa

   S A S V G D R V T I T C ] [ K T S Q D I
                                CDR1

163 aacaagtatatggcttggtaccaaCAGACAcctggaaaaGCTcctaggctgtc
   -----
   ttgttcataataccgaaccatgggtGTCTGTggaccttttCGAggatccgacgag

   N K Y M A ] [ W Y Q Q T P G K A P R L L
                                FR2

217 atacattacacatctgcattacagccaggcatcccatcaagggttcagtggaagt
   -----
   tatgtaatgtgtagacgtaatgtcggtccgtagggtagttccaagtcaccttca

   I H ] [ Y T S A L Q P ] [ G I P S R F S G S
                                CDR2

271 gggctctgggagagatttatACTttcACCAcagcAGCctgCAGcctgaagatatt
   -----
   cccagaccctctctaataTGAAagTGGtagtcgTCGgacGTCggacttctataa

   G S F R D Y T F T I S S L Q P E D I
                                FR3
  
```

FIG. 15A

325 gcaacttattattgtctacagtatgataatctgtggacggtcggtCAAggcacc

cggtgaataataacagatgtcatactattagacacctgcaagccaGTTccgtgg

A T Y Y C)[L Q Y D N L W T][F G Q G T
CDR3 FR4

SPLICE DONOR SITE BamHI
aagGTGgaaatcaaacgtgagtgatcc
379 -----
ttcCACcttttagtttgactcacctagg

K V E I K]

FIG. 15B

HindIII KOZAK SEQUENCE
AAGCTTGCCGCCACCATGGACTGGACCTGGCGCGTGTTTTGCCTGCTCGCCGTG
1 -----
TTCGAACGGCGGTGGTACCTGACCTGGACCGCGCACAAAACGGACGAGCGGCAC

[M D W T W R V F C L L A V
LEADER

GCTCCTGGGGCCACAGCCAGGTGCAACTAGTGCAGTCCGGCGCCGAAGTGAAG
55 -----
CGAGGACCCCGGGTGTCTGGTCCACGTTGATCACGTCAGGCCGCGGCTTCACTTC

A P G A H S][Q V Q L V Q S G A E V K

AAACCCGGTGCTTCCGTGAAAGTCAGCTGTAAAGCTAGCGGTttcaacattaaa
109 -----
TTTGGGCCACGAAGGCACTTTTCAGTCGACATTTCGATCGCCAAagttgtaattt

K P G A S V K V S C K A S G F N I K][
FR1

gacacctatatacactGGGTTAGACAGGCCCCctGGCCAAaGGCTgGAGTGGATg
163 -----
ctgtggatatatgtgACCCAATCTGTCCGGgGaCCGGTTtCCGAcCTCACCTAC

D T Y I H][W V R Q A P G Q R L E W M
CDR1 FR2

FIG. 16A

217 GGaaggattgatcctgcgaatggttataactaaatatgacccgaagtccagggc

CCttcctaactaggacgcttaccaatatgatttatactgggcttcaaggtcccg
G)[R I D P A N G Y T K Y D P K F Q G)]
CDR2

271 cgggtcACCatcACCGcaGACACCTCTgccagcACCGCCTACATGGAAGTGTCC

gcccagTGGtagTGGcgtCTGTGGAGAcggtcgtTGGCGGATGTACCTTGACAGG
R V T I T A D T S A S T A Y M E L S
FR3

325 AGCCTGCGCTCCGAGGACACTGCAGTCTACTACTGCGCCagagagggatattat

TCGGACGCGAGGCTCCTGTGACGTCAGATGATGACGCGGtctctccctataata
S L R S E D T A V Y Y C A R)](E G Y Y
ggtaactacggggtctatgctatgGACTAcTGGGGtCAaGGaACCCTTGTCACC

ccattgatgccccagatacagatacCTGATgACCCCaGTtCCtTGGGAACAGTGG
379
G N Y G V Y A M D Y)](W G Q G T L V T
CDR3 FR4

SPLICE DONOR SITE BamHI
GTctccTCAGGTGAGTGGATCC

433 CAGaggAGTCCACTCACCTAGG
V S S]

FIG. 16B

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Leu Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Asp Ile Ser Asn
Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gly Ser Pro Lys Leu Leu
Ile Tyr Tyr Ala Ser Arg Leu His Ser Gly Val Pro Ser Arg Phe Ser
Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu
Gln Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro
Pro Arg Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys - C

FIG. 17A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Asp Ser Leu Val Xaa
Xaa Ser Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Gly Lys
Ala Pro Lys Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr
Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
Tyr Asn Ser Leu Pro Glu Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
Ile Lys - C

FIG. 17B

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys Pro Gly Ala
Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr
Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile
Gly Arg Ile Asp Pro Ala Asn Gly Asn Thr Lys Tyr Asp Pro Lys Phe
Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
Ala Arg Gly Tyr Tyr Tyr Tyr Asp Ser Xaa Val Gly Tyr Tyr Ala Met
Asp Tyr Trp Gly Gln Gly Thr Xaa Val Thr Val Ser Ser - C

FIG. 18A

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

N - Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly Ala
Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr
Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp Met
Gly Trp Ile Asn Pro Tyr Gly Asn Gly Asp Thr Asn Tyr Ala Gln Lys
Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
Cys Ala Arg Ala Pro Gly Tyr Gly Ser Gly Gly Gly Cys Tyr Arg Gly Asp
Tyr Xaa Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser - C

FIG. 18B